

P5

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/891,053

DATE: 10/04/2001

TIME: 08:18:55

Input Set : A:\06501-083001.TXT

Output Set: N:\CRF3\10042001\I891053.raw

ENTERED

4 <110> APPLICANT: Itadani, Hiraku
5 Takimura, Tetsuo
6 Nakamura, Takao
7 Kobayashi, Masahiko
8 Tanaka, Ken-ichi
9 Hidaka, Yusuke
10 Ohta, Masataka
13 <120> TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
14 BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
17 <130> FILE REFERENCE: 06501-083001
19 <140> CURRENT APPLICATION NUMBER: 09/891,053
C--> 20 <141> CURRENT FILING DATE: 2001-09-17
22 <150> PRIOR APPLICATION NUMBER: PCT/JP99/07280
23 <151> PRIOR FILING DATE: 1999-12-24
25 <150> PRIOR APPLICATION NUMBER: PCT/JP98/05967
26 <151> PRIOR FILING DATE: 1998-12-25
28 <150> PRIOR APPLICATION NUMBER: JP 11/145661
29 <151> PRIOR FILING DATE: 1999-05-25
31 <160> NUMBER OF SEQ ID NOS: 26
33 <170> SOFTWARE: FastSEQ for Windows Version 4.0
35 <210> SEQ ID NO: 1
36 <211> LENGTH: 413
37 <212> TYPE: PRT
38 <213> ORGANISM: Rattus norvegicus
40 <400> SEQUENCE: 1
41 Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
42 1 5 10 15
43 Ala Gly Glu Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
44 20 25 30
45 Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
46 35 40 45
47 Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
48 50 55 60
49 Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
50 65 70 75 80
51 Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
52 85 90 95
53 Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
54 100 105 110
55 Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile
56 115 120 125
57 Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala
58 130 135 140
59 Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp
60 145 150 155 160
61 Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr
62 165 170 175

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```

63 Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe
64           180           185           190
65 Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe
66           195           200           205
67 Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn
68           210           215           220
69 Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly
70 225           230           235           240
71 Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Ala Pro Pro
72           245           250           255
73 Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu
74           260           265           270
75 His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu
76           275           280           285
77 Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg
78           290           295           300
79 Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg
80 305           310           315           320
81 Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly
82           325           330           335
83 Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys
84           340           345           350
85 His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu
86           355           360           365
87 Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His
88           370           375           380
89 Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu
90 385           390           395           400
91 Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys
92           405           410

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94 <210> SEQ ID NO: 2

95 <211> LENGTH: 1239

96 <212> TYPE: DNA

97 <213> ORGANISM: Rattus norvegicus

99 <220> FEATURE:

100 <221> NAME/KEY: CDS

101 <222> LOCATION: (1)...(1239)

103 <400> SEQUENCE: 2

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104 atg gag cgc gcg ccg ccc gac ggg ctg atg aac gcg tcg ggc act ctg      48
105 Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
106 1           5           10           15
108 gcc gga gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc      96
109 Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
110           20           25           30
112 tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca      144
113 Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
114           35           40           45
116 gta ctg ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc      192
117 Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser

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118	50	55	60	
120	ctc cgc acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac	240		
121	Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp			
122	65 70 75 80			
124	ttc ctc gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg	288		
125	Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu			
126	85 90 95			
128	acc ggc cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg	336		
129	Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val			
130	100 105 110			
132	gta gac tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc	384		
133	Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile			
134	115 120 125			
136	agc tat gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc	432		
137	Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala			
138	130 135 140			
140	cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg	480		
141	Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp			
142	145 150 155 160			
144	gtg ctg gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac	528		
145	Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr			
146	165 170 175			
148	ctg tct ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc	576		
149	Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe			
150	180 185 190			
152	ttc tac aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc	624		
153	Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe			
154	195 200 205			
156	acg ccc ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac	672		
157	Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn			
158	210 215 220			
160	atc cag agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc	720		
161	Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly			
162	225 230 235 240			
164	cca gaa ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc	768		
165	Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro			
166	245 250 255			
168	agc tgc tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg	816		
169	Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu			
170	260 265 270			
172	cac agc tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc	864		
173	His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu			
174	275 280 285			
176	aaa agg ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc	912		
177	Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg			
178	290 295 300			
180	atg aag atg gtg tcc cag agc atc acc cag cgc ttc cgg ctg tcg cgg	960		
181	Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg			
182	305 310 315 320			

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```

184 gac aag aag gtg gcc aag tcg ctg gcc atc atc gtg agc atc ttt ggg      1008
185 Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly
186                               325                               330                               335
188 ctc tgc tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc      1056
189 Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys
190                               340                               345                               350
192 cat ggc cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt      1104
193 His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu
194                               355                               360                               365
196 ctg tgg gcc aac tcg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac      1152
197 Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His
198                               370                               375                               380
200 tac agc ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc      1200
201 Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu
202 385                               390                               395                               400
204 aag gtc cag ccc cac ggc tcc ctg gag cag tgc tgg aag      1239
205 Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys
206                               405                               410

```

```

209 <210> SEQ ID NO: 3
210 <211> LENGTH: 21
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
215 <223> OTHER INFORMATION: artificially synthesized primer sequence
217 <221> NAME/KEY: misc_feature
218 <222> LOCATION: (1)...(21)
219 <223> OTHER INFORMATION: n = A,T,C or G
221 <400> SEQUENCE: 3

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W--> 222 batngccaac ctbkccttct c 21

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224 <210> SEQ ID NO: 4
225 <211> LENGTH: 20
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: artificially synthesized primer sequence
232 <221> NAME/KEY: misc_feature
233 <222> LOCATION: (1)...(20)
234 <223> OTHER INFORMATION: n = A,T,C or G
236 <400> SEQUENCE: 4

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W--> 237 ccataaaaagn nggggttgac 20

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239 <210> SEQ ID NO: 5
240 <211> LENGTH: 2700
241 <212> TYPE: DNA
242 <213> ORGANISM: Rattus norvegicus
244 <220> FEATURE:
245 <221> NAME/KEY: CDS
246 <222> LOCATION: (351)...(1589)
248 <221> NAME/KEY: misc_feature
249 <222> LOCATION: (1)...(2700)

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Input Set : A:\06501-083001.TXT

Output Set: N:\CRF3\10042001\I891053.raw

```

250 <223> OTHER INFORMATION: n = A,T,C or G
252 <400> SEQUENCE: 5
253 aattcggcac gagcgggcag atcgcggggc gcaactcggtt gcgcgctgag ctaggggtgc      60
254 accgacgcac cgcgggcggc tggagctcgg ctttgccttc gctgcagcag cgcgcgcgcc      120
255 cgcgggcactc cgctcagatt ccgacaccag cccctcttgg atcgccctcc tggactctag      180
256 cccgggctct tgctccgacc ccgcggacca tgctccgggc gcccccggga aaaccgggct      240
257 gggcgaagag ccggcaaaga ttaggtcac gagcgggggc cccacccggc caccagctc      300
258 tccgcccgtg cctgcccgg tgccccgag ccgtgtgagc ctgctgggcc atg gag      356
259                                     Met Glu
260                                     1
262 cgc gcg ccg ccc gac ggg ctg atg aac gcg tcg ggc act ctg gcc gga      404
263 Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu Ala Gly
264         5                10                15
266 gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc tgg acc      452
267 Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala Trp Thr
268         20                25                30
270 gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca gta ctg      500
271 Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr Val Leu
272         35                40                45                50
274 ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc ctc cgc      548
275 Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser Leu Arg
276         55                60                65
278 acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac ttc ctc      596
279 Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp Phe Leu
280         70                75                80
282 gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg acc ggc      644
283 Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu Thr Gly
284         85                90                95
286 cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg gta gac      692
287 Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val Val Asp
288         100               105               110
290 tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc agc tat      740
291 Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile Ser Tyr
292 115                120                125                130
294 gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc cag cag      788
295 Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln
296         135               140               145
298 ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg gtg ctg      836
299 Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp Val Leu
300         150               155               160
302 gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac ctg tct      884
303 Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser
304         165               170               175
306 ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc ttc tac      932
307 Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe Phe Tyr
308         180               185               190
310 aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc acg ccc      980
311 Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe Thr Pro
312 195                200                205                210

```

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\06501-083001.TXT

Output Set: N:\CRF3\10042001\I891053.raw

L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

L:383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11

L:823 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22

L:838 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23